REMARKS

Reconsideration is requested.

Claims 1-44 have been canceled without prejudice. Claims 45-56 are pending. No new matter has been added.

Attached is an Information Disclosure Statement with a PTO 1449 listing references previously cited but not considered as well as additional references of record, and not previously cited herein, in the copending related application Serial Nos. 09/638,693; 09/873,224 and 09/878,281. Copies of the pending claims from these related copending applications are attached. Consideration of the attached and return of an initialed copy of the attached PTO 1449 Form, pursuant to MPEP § 609, are requested.

The Examiner is requested to acknowledge receipt by the Patent Office of the priority documents in the grand-parent application Serial No. 08/362,455, from the International Bureau with regard to PCT/EP94/01323, as evidenced by the attached Notification of Acceptance dated February 10, 1995. The Examiner is further requested to acknowledge the applicants claim to domestic priority.

The specification has been amended to include the heading "Brief Description of the Drawings" as suggested by the Examiner on page 3 of the Office Action dated December 3, 2003 (Paper No. 12). The applicants note that the undersigned's filing coversheet dated July 6, 2001, requested an amendment of the specification on page 1, before the first line, to include the following: "This application is a division of Application No. 08/362,455, filed January 11, 1995, , the entire content of which is hereby

incorporated by reference in this application." The specification has been further amended above to also refer to the International Application. The Examiner is requested to ensure this amendment is entered in the application or advise the undersigned in the event anything further is required in this regard.

The specification has been amended to include the attached Sequence Listing as well as sequence identifiers corresponding therewith. A similar amendment has been made and entered in the copending related application Serial No. 09/878,281.

Page 33 has been amended above to correct an inadvertent typographical error. Support for the amendment may be found in, for example, Figure 5.

The applicants further note that page 39 has been amended as shown above to be consistent with amendments made in the related application Serial No. 09/638,693, and specifically, the applicants note that SEQ ID NOs:166, 168 etc., are mentioned on page 39 (penultimate and last bulleted point) of the description. SEQ ID NO:168 for instance has the sequence TCGF.....HRMA, as described in the Sequence Listing. Figure 5 indicates that the first amino acid T (thr) corresponds to amino acid 127 of the HCV polyprotein. Likewise, the last amino acid A (ala) of SEQ ID NO:168 corresponds to amino acid 319 of the HCV polyprotein (see Figure 5). The HCV Core protein spans positions 1-191 of the HCV polyprotein, the HCV E1 protein spans positions 192-383 of the HCV polyprotein. As SEQ ID NO:168 (and all other sequences of claim 87) starts at position 127, it will be understood to contain part of the Core protein. Hence, these sequences are to be regarded as Core/E1 proteins, as amended above. SEQ ID NO:166 is one of the sequences aligned in Figure 5 and spans amino acids 1-126 of the HCV polyprotein (MSTN.....IDTL) in accordance with SEQ ID

NO:166 in Sequence Listing. As the HCV Core protein spans positions 1-191 of the HCV polyprotein, SEQ ID NO:166 will be recognized by one of ordinary skill in the art as a Core protein, as amended above.

Page 40 (1st bulleted point) of the description has been amended above with regard to SEQ ID NO:192, which the Examiner will appreciate has the sequence MSTN.....WAGW, as described in the Sequence Listing. As will be clear from the description above with regard to SEQ ID NO:166, "MSTN...." refers to the start of the HCV polyprotein Core. SEQ ID NO:192 can be allocated amino acids 1-96 of the HCV Core polyprotein based on the sequence alignments in Figure 5. SEQ ID NO:192 is moreover one of the sequences aligned in Figure 5.

The specification has been further amended above on page 40 with regard to SEQ ID NOs:198 and 200. SEQ ID NOs:198 and 200 both cover the sequence CARTITT.....W(X/A)TY, as described in the Sequence Listing. SEQ ID NO:270 covers the sequence TITT.....WATY. SEQ ID NO:270 is one of the sequences aligned in Figure 7 (except for the first amino acid "T") and from Figure 7 one of ordinary skill in the art will appreciate that SEQ ID NO:270 spans amino acids 1284-1764 of the HCV polyprotein. SEQ ID NOs:198 and 200 both have 3 extra amino acids at their amino-terminus and thus span amino acids 1281-1764 of the HCV polyprotein. The common amino acids for the three SEQ ID NOs are 1284-1764.

A replacement sheet 4 of 111 of the Figures is attached to correct inadvertent notations apparently made during prosecution of the parent application and not removed prior to copying of the application and filing of the present application. No new matter has been added.

The attached paper and computer readable copies of the Sequence Listing are the same. No new matter has been added. A separate Statement to this effect is attached.

The objections to claims 24, 26 and 30-32 noted on page 3 of Paper No. 12 are moot in view of the above. The claims have been drafted above with the Examiner's concerns in mind.

The Rule 75 objection to claim 40 is moot in view of the above amendments.

The Section 112, first paragraph, rejection of claims 33, 37, 38, 40, 43 and 44 is moot in view of the above. The pending claims are submitted to be supported by an enabling disclosure.

The Section 112, second paragraph, rejection of claims 24-39 is moot in view of the above. The pending claims are submitted to be definite. The applicants submit that the recitation of "specifically recognizing" will be recognized by one of ordinary skill in the art as requiring an antibody that binds only to an HCV type 3 antigen and does not bind to antigen from another HCV type.

The Section 103 rejection of claims 24, 25, 27, 28, 30, 31 and 41 over Cha (WO92/19743) "in light of Applicant's admission in the specification at Table 3, page 11" is moot. Similarly, the Section 103 rejection of claims 26, 29, 32, 35, 36, 41, 42, 34, 38 and 39 in view of Cha, the "Applicant's admission" and Co (PNAS 88(7):2869-2973 (1991)) is moot. The claims are submitted to be patentable over the combination of art. Specifically, the applicants submit that Cha, if relevant at all to the presently claimed invention (Cha fails to disclose amino acid sequences, as admitted by the Examiner on page 6 of Paper No. 12), discloses sequences relating to type GIV (corresponding to

type 3a), as indicated by the Examiner. More particularly, Cha disclosed in Figure 3 sequences of an "envelope region". However, translation of SEQ ID NO:23 yields a protein spanning amino acids 330-362 of the E1 region. The other SEQ ID NO:5 in Figure 3 cover the same region. This E1 region is outside the presently claimed range. The claims are submitted to be patentable over the cited art.

The claims are submitted to be in condition for allowance and a Notice to that effect is requested. The Examiner is urged to contact the undersigned, preferably by telephone, in the event anything further is required.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____

B. J. Sadoff
Reg. No. 36,663

BJS:pp
1100 North Glebe Road, 8th Floor
Arlington, VA 22201-4714
Telephone: (703) 816-4000
Facsimile: (703) 816-4100

56. (Previously Presented) An isolated polypeptide or peptide comprising or more contiguous amino acids selected from at least one HCV polypeptide or peptide selected from the group consisting of:

an HCV type 3a polypeptide or peptide selected from the region spanning positions 140 to 319 of the Core/E1 region of HCV type 3a;

an HCV type 3a polypeptide or peptide selected from the region spanning positions 1556 to 1650 of the NS3/NS4 region of HCV type 3a;

an HCV type 3a polypeptide or peptide selected from the region spanning positions 1646 to 1764 of the NS3/NS4 region of HCV type 3a;

an HCV type 4 polypeptide or peptide selected from the region spanning positions 127 to 319 of the Core/E1 region of HCV type 4;

an HCV type 4 polypeptide or peptide selected from the region spanning positions 192 to 319 of the E1 region of HCV type 4;

an HCV type 4 polypeptide or peptide selected from the region spanning positions 2645 to 2757 of the NS5B region of HCV type 4;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 1 to 191 of the Core region of HCV type 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 192 to 319 of the E1 region of HCV type 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 1 to 319 of the Core/E1 region of HCV type 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 308 to 503 of the E1/E2 region of HCV type 5;

an HCV subtype 5 polypeptide or peptide selected from the region spanning positions 1286 to 1403 of the NS3 region of HCV subtype 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 1646 to 1764 of the NS3/NS4 region of HCV type 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 1284 to 1764 of the NS3/NS4 region of HCV type 5;

an HCV type 5 polypeptide or peptide selected from the region spanning positions 2645 to 2757 of the NS5 region of HCV type 5;

an HCV subtype 2d polypeptide or peptide selected from the region spanning positions 1 to 319 of the Core/E1 region of HCV subtype 2d;

an HCV subtype 2d polypeptide or peptide selected from the region spanning positions 192 to 319 of the E1 region of HCV subtype 2d;

an HCV subtype 2d polypeptide or peptide selected from the region spanning positions 2645 to 2757 of the NS5B region of HCV subtype 2d;

wherein said peptide or polypeptide contains at least one genotype-specific amino acid.

57. (Previously Presented) An HCV type 5 polypeptide or peptide selected from the region spanning positions 1 to 2757 of HCV type 5, and wherein said peptide or polypeptide is obtainable by amplification of HCV type 5 specific polynucleic acids using HCV type 5 specific primers,

and wherein said peptide or polypeptide contains at least one genotype-specific amino acid.

58. (Previously Presented) An isolated HCV type 3a polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 14, 16, 18, 20, or 24,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 140 to 319 of the Core/E1 region of HCV type 3a.

59. (Previously Presented) An isolated HCV type 3a polypeptide comprising an amino acid sequence or peptide selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 32, 36, or 223,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1646 to 1764 of the NS3/NS4 region of HCV type 3a.

60. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 123,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 127 to 317 of the Core/E1 region of HCV type 4.

61. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 168, 170, 172, 174, 176, 178, 180, 182, 186, 188 or 190

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 192 to 319 of the E1 region of HCV type 4.

62. (Previously Presented) An isolated HCV type 4 polypeptide or peptide selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 107, 109, 111, 113, 115, 117, 202, 204, 208, 210 or 212,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 2645 to 2757 of the NS5B region of HCV type 4.

63. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 164 or 194,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 166 of the Core/E1 region of HCV type 4.

64. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 50, or 52,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 191 of the Core region of HCV type 5.

65. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 50, 52, 152, or 156

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 192 to 319 of the E1 region of HCV type 5.

66. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 50, or 52,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 319 of the Core/E1 region of HCV type 5.

67. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptide or peptide of SEQ ID NO: 158,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 308 to 503 of the E1/E2 region of HCV type 5.

68. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 56, or 58,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1286 to 1403 of the NS3 region of HCV type 5.

69. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 60, or 62,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1646 to 1746 of the NS3/NS4 region of HCV type 5.

70. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 160 or 162,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 2645 to 2757 of the NS5 region of HCV type 5.

71. (Previously Presented) An isolated HCV subtype 2d polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 144,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 319 of the Core/E1 region of HCV subtype 2d.

72. (Previously Presented) An isolated HCV subtype 2d polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptide or peptide of SEQ ID NO: 144,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 192 to 319 of the E1 region of HCV subtype 2d.

73. (Previously Presented) An isolated HCV subtype 2d polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptide or peptide of SEQ ID NO: 146,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 2645 to 2757 of the NS5B region of HCV subtype 2d.

74. (Previously Presented) An isolated HCV polypeptide or peptide according to any of claims 56 or 57, which contains in its sequence at least one of the following amino acid residues:

L7, M44, R67, Q70, A79, A87, N106, K115, A127, A190, S130, V134, G142, I144, E152, A157, V158, P165, S177 or Y177, I178, V180 or E180, R184, I186, H187, T189, A190, S191, Q192 or I192 or E192, N193 or H193 or P193, W194, H195, A197, Q208, A210, V212, F214, R217 or D217 or V217, H218 or N218, H219 or L219, L227 or I227, M231 or E231 or Q231, A232 or K232, I235, A237 or T237, I242, I246, S247, S248, V249, S250, I251 or V251 or M251 or F251, D252, V254, L255 or V255, E256, M258 or F258 or V258, Q260 or S260, A261, T264 or Y264, M265, I266 or A266, A267, G268 or T268, F271 or M271, I277, M280 or H280, A284, V274, N292 or S292, I293 or Y293, Q294, L297 or I297 or Q297, A299 or K299 or Q299, N303, T308 or L308, T310 or F310 or A310 or D310 or V310, L313, G317 or Q317, L333, S351, A358, A359, A363, S364, A366, T369, L373, F376, Q386, I387, S392, I399, F402, I403,

R405, D454, A461, A463, T464, K484, Q500, E501, S521, K522, H524, N528, S531, S532, V534, F536, M539, I546, H1310, V1312, Q1321, P1368, V1373, K1405, Q1406, A1424, A1429, C1435, S1436, S1456, H1496, A1504, D1510, D1529, I1543, N1567, D1556, N1567, M1572, Q1579, L1581, S1583, F1585, V1595, E1606 or T1606, M1611, V1612 or L1612, P1630, C1636, T1656 or I1656, L1663, V1667, V1677, A1681, H1685, E1687, G1689, V1695, A1700, Q1704, Y1705, A1713, A1714 or S1714, M1718, D1719, A1721 or T1721, R1722, A1723 or V1723, H1726 or G1726, E1730, V1732, F1735, I1736, S1737, R1738, T1739, G1740, Q1741, K1742, Q1743, A1744, T1745, L1746, E1747 or K1747, I1749, A1750, T1751 or A1751, V1753, N1755, K1756, A1757, P1758, A1759, H1762, T1763, Y1764, P2645, A2647, K2650, K2653 or L2653, S2664, N2673, F2680, K2681, L2686, Q2695 or L2695 or I2695, V2712, F2715, V2719 or Q2719, T2722, T2724, S2725, R2726, G2729, Y2735, H2739, G2746 or I2746, 12748, P2752 or K2752, P2754 or T2754, T2757 or P2757.

75. (Previously Presented) A polypeptide or peptide according to any of claims 56 or 57, wherein said polypeptide or peptide is selected from the following peptides:

QPTGRSWGQ	(SEQ ID NO 93)
RSEGRTSWAQ	(SEQ ID NO 220)
RTEGRTSWAQ	(SEQ ID NO 221)
LEWRNTSGLYVL	(SEQ ID NO 83)
VNYRNASGIYHI	(SEQ ID NO 126)

QHYRNISGIYHV	(SEQ ID NO 127)
EHYRNASGIYHI	(SEQ ID NO 128)
IHYRNASGIYHI	(SEQ ID NO 224)
VPYRNASGIYHV	(SEQ ID NO 84)
VNYRNASGIYHI	(SEQ ID NO 225)
VNYRNASGVYHI	(SEQ ID NO 226)
QHYRNASGIYHV	(SEQ ID NO 228)
QHYRNVSGIYHV	(SEQ ID NO 229)
IHYRNASDGYYI	(SEQ ID NO 230)
LQVKNTSSSYMV	(SEQ ID NO 231)
VYEADDVILHT	(SEQ ID NO 85)
VYETEHHILHL	(SEQ ID NO 129)
VYEADHHIMHL	(SEQ ID NO 130)
VYETDHHILHL	(SEQ ID NO 131)
VYEADNLILHA	(SEQ ID NO 86)
VYEADYHILHL	(SEQ ID NO 233)
VYETDNHILHL	(SEQ ID NO 234)
VYETENHILHL	(SEQ ID NO 235)
VFETDHHIMHL	(SEQ ID NO 238)
VYETENHILHL	(SEQ ID NO 239)
VQDGNTSTCWTPV	(SEQ ID NO 87)
VQDGNTSACWTPV	(SEQ ID NO 241)
VRVGNQSRCWVAL	(SEQ ID NO 132)

VRTGNTSRCWVPL	(SEQ ID NO 133)
VRAGNVSRCWTPV	(SEQ ID NO 134)
EEKGNISRCWIPV	(SEQ ID NO 242)
VKTGNQSRCWVAL	(SEQ ID NO 243)
VRTGNQSRCWVAL	(SEQ ID NO 244)
VKTGNVSRCWISL	(SEQ ID NO 248)
VRKDNVSRCWVQI	(SEQ ID NO 249)
VRYVGATTAS	(SEQ ID NO 89)
APYIGAPLES	(SEQ ID NO 135)
APYVGAPLES	(SEQ ID NO 136)
AVSMDAPLES	(SEQ ID NO 137)
APSLGAVTAP	(SEQ ID NO 90)
APSFGAVTAP	(SEQ ID NO 250)
VSQPGALTKG	(SEQ ID NO 251)
VKYVGATTAS	(SEQ ID NO 252)
APYIGAPVES	(SEQ ID NO 253)
AQHLNAPLES	(SEQ ID NO 254)
SPYVGAPLEP	(SEQ ID NO 255)
SPYAGAPLEP	(SEQ ID NO 256)
APYLGAPLEP	(SEQ ID NO 257)
APYLGAPLES	(SEQ ID NO 258)
APYVGAPLES	(SEQ ID NO 259)
VPYLGAPLTS	(SEQ ID NO 260)

APHLRAPLSS	(SEQ ID NO 261)
APYLGAPLTS	(SEQ ID NO 262)
RPRRHQTVQT	(SEQ ID NO 91)
QPRRHWTTQD	(SEQ ID NO 138)
RPRRHWTTQD	(SEQ ID NO 139)
RPRQHATVQN	(SEQ ID NO 92)
RPRQHATVQD	(SEQ ID NO 263)
SPQHHKFVQD	(SEQ ID NO 264).

76. (Previously Presented) A composition comprising an isolated polypeptide or peptide according to any of claims 56 or 57.

77. (Previous Presented) A method for raising antibodies comprising administering a polypeptide or peptide according to any of claims 56 or 57 to a mammal.

78. (Previously Presented) A method of detecting, screening or confirmation for the presence of HCV antibodies present in a biological sample, comprising the following steps:

(i) providing a sample suspected of containing HCV antibody,

(ii) contacting the sample with a polypeptide or peptide according to any of claims 56 or 57, under appropriate conditions allowing the formation of an immune complex,

(iii) inferring from the presence of the immune complex of step (ii) the presence of HCV antibodies in said sample.

79. (Previously Presented) A method of detecting, screening or confirmation for one or more HCV serotypes present in a biological sample, comprising the following steps:

(i) providing a sample suspected of containing HCV antibody,

(ii) contacting the sample with a polypeptide or peptide according to any of claims 56 or 57, under appropriate conditions allowing the formation of an immune complex,

(iii) inferring from the presence of one or more of these immune complexes of step (ii) the serotype(s) present in said sample.

80. (Previously Presented) A method for detecting HCV serotype(s) present in a biological sample liable to contain it, comprising at least the following steps:

(i) contacting the biological sample to be analyzed for the presence of HCV antibodies with at least one peptide or polypeptide according to any of claims 56 or 57, preferentially in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide or peptide is preferentially in the form of a biotinylated polypeptide or peptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes,

(ii) removing unbound components,

(iii) incubating the immune complexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,

(iv) detecting the presence of said immune complexes visually or by means of densitometry and inferring the HCV serotype(s) present from the observed binding pattern.

81. (Previously Presented) A method for confirmation of HCV serotype(s) present in a biological sample liable to contain it, comprising at least the following steps:

(i) contacting the biological sample to be analyzed for the presence of HCV antibodies with at least one peptide or polypeptide according to any of claims 56 or 57, preferentially in an immobilized form under appropriate conditions which allow the formation of an immune complex, wherein said polypeptide or peptide is preferentially in the form of a biotinylated polypeptide or peptide and is covalently bound to a solid substrate by means of streptavidin or avidin complexes,

(ii) removing unbound components,

(iii) incubating the immune complexes formed with heterologous antibodies, which specifically bind to the antibodies present in the sample to be

analyzed, with said heterologous antibodies having conjugated to a detectable label under appropriate conditions,

(iv) detecting the presence of said immune complexes visually or by means of densitometry and confirm the HCV serotype(s) present from the observed binding pattern.

82. (Previously Presented) A kit for detecting, screening or confirmation for one or more HCV serotype(s) present in a biological sample, comprising:

(i) a polypeptide or peptide according to any of claims 56 or 57,

(ii) possibly a buffer and components necessary for producing the formation of an immune complex,

(iii) optionally a means for detecting, screening or confirming the immune complex(es) formed.

83. (Previously Presented) A kit for detecting, screening or confirmation for the presence of HCV antibodies present in a biological sample, comprising:

(i) a polypeptide or peptide according to any of claims 56 or 57,

(ii) possibly a buffer and components necessary for producing the formation of an immune complex,

(iii) optionally a means for detecting, screening or confirming the immune complex formed.

84. (Previously Presented) A kit for detecting HCV serotype(s) present in a biological sample liable to contain it, comprising at least the following components:

(i) at least a polypeptide or peptide according to any of claims 56 or 57, with said polypeptide or peptide being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,

(ii) a buffer and components necessary for producing the buffer enabling binding reaction between these polypeptides or peptides and the antibodies against HCV present in the biological sample,

(iii) optionally, a detector for determining the presence of immune complexes formed in the preceding binding reaction, and

(iv) optionally an automated scanning and interpretation device to confirm the HCV serotype(s) present in the sample from the observed binding pattern.

85. (Previously Presented) A kit for confirmation of HCV serotype(s) present in a biological sample liable to contain it, comprising at least the following components:

(i) at least a polypeptide or peptide according to any of claims 56 or 57, with said polypeptide or peptide being preferentially immobilized on a solid substrate, and more preferentially on one and the same membrane strip,

(ii) a buffer and components necessary for producing the buffer enabling binding reaction between these polypeptides or peptides and the antibodies against HCV present in the biological sample,

(iii) optionally, a detector for determining the presence of immune complexes formed in the preceding binding reaction, and

(iv) optionally, an automated scanning and interpretation device to confirm the HCV serotype(s) present in the sample from the observed binding pattern.

86. (Previously Presented) An isolated HCV type 3a polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptide or peptide of SEQ ID NO: 30,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1556 to 1650 of the NS3/NS4 region of HCV type 3a.

87. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 168, 170, 172, 174, 176, 178, 180, 182, 186, 188, or 190

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 127 to 319 of the Core/E1 region of HCV type 4.

88. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 166,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 126 of the Core region of HCV type 4.

89. (Previously Presented) An isolated HCV type 4 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 192,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1 to 96 of the Core region of HCV type 4.

90. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 156,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 127 to 319 of the Core/E1 region of HCV type 5.

91. (Previously Presented) An isolated HCV type 5 polypeptide or peptide comprising an amino acid sequence selected from the group consisting of

(i) the polypeptides or peptides of SEQ ID NO: 198, 200, or 270,

(ii) at least 5 amino acids from the polypeptide or peptide of (i) having at least one genotype-specific amino acid from the region spanning positions 1284 to 1764 of the NS3/NS4 region of HCV type 5.

24. (Previously Presented) An isolated polynucleic acid sequence consisting of 8 or more contiguous nucleotides selected from an HCV subtype 3c genomic sequence, wherein said polynucleic acid sequence is capable of hybridizing to HCV type 3c, but not another type or subtype of HCV; or

the complement of said polynucleic acid, wherein said polynucleic acid contains at least one genotype 3c-specific nucleotide.

25. (Previously Presented) An isolated Hepatitis C virus polynucleic acid selected from the group consisting of:

(i) the nucleotide sequence of SEQ ID NO:147,

(ii) at least 8 contiguous nucleotides of a nucleotide sequence having at least one genotype-specific nucleotide from the region spanning positions 1 to 957 of the Core or Core/E1 region of HCV subtype 3c, and,

(iii) the complement of the nucleotide sequence of (i) or (ii).

26. (Previously Presented) A recombinant vector comprising a vector sequence and a prokaryotic, eukaryotic or viral promotor sequence operably linked to a polynucleic acid sequence of claim 24.

27. (Previously Presented) A recombinant vector comprising a vector sequence and a prokaryotic, eukaryotic or viral promotor sequence operably linked to a polynucleic acid sequence of claim 25.

28. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the presence of a polynucleic acid sequence according to claim 24, by means of a sequencing reaction, and,

(iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

29. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the presence of a polynucleic acid sequence according to claim 25, by means of a sequencing reaction, and,

(iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

30. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) specifically amplifying a polynucleic acid sequence according to claim 24, and,

(iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

31. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) specifically amplifying a polynucleic acid sequence according to claim 25, and,

(iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

32. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a primer for specific amplification for HCV type- or subtype-specific amplification.

33. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a primer for specific amplification for HCV type- or subtype-specific amplification.

34. (Previously Presented) An isolated HCV polynucleic acid according

to claim 24, wherein said polynucleic acid is capable of acting as a primer for specific amplification of a HCV subtype 3c nucleic acid sequence.

35. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a primer for specific amplification of a HCV subtype 3c nucleic acid sequence.

36. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV type or subtype-specific hybridization.

37. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV type or subtype-specific hybridization.

38. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV subtype 3c nucleic acid sequence.

39. (Previously Presented) An isolated HCV polynucleic acid according to claim 25, wherein said polynucleic acid is capable of acting as a probe for specific hybridization to a HCV subtype 3c nucleic acid sequence.

40. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a polynucleic acid sequence according to claim 24.

41. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a polynucleic acid sequence according to claim 25.

42. (Previously Presented A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 32.

43. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 33.

44. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 34.

45. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a primer according to claim 35.

46. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 36.

47. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 37.

48. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 38.

49. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a solid support and a probe according to claim 39.

50. (Previously Presented A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 32, (iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the

observed pattern of amplified fragments.

51. (Previously Presented A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 33, (iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the

observed pattern of amplified fragments.

52. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 34, (iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the

observed pattern of amplified fragments.

53. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(i) providing a sample nucleic acid,

(ii) amplifying the nucleic acid with at least one primer according to claim 35, (iii) detecting the amplified nucleic acids,

(iv) inferring the presence of one or more genotypes of HCV present from the

observed pattern of amplified fragments.

54. (Previously Presented) A method for determining the presence of

HCV genotypes present in a biological sample comprising the steps of:

(ii) providing a sample nucleic acid,

(iii) optionally amplifying the nucleic acid with at least one primer,

(iv) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 36, with said probes being optionally attached to a solid substrate,

(v) optionally washing,

(vi) detecting the hybrids formed,

(vii) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

55. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(ii) providing a sample nucleic acid,

(iii) optionally amplifying the nucleic acid with at least one primer,

(iv) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 37, with said probes being optionally attached to a solid substrate,

(v) optionally washing,

(vi) detecting the hybrids formed,

(vii) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

56. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(ii) providing a sample nucleic acid,

(iii) optionally amplifying the nucleic acid with at least one primer,

(iv) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 38, with said probes being optionally attached to a solid substrate,

(v) optionally washing,

(vi) detecting the hybrids formed,

(vii) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

57. (Previously Presented) A method for determining the presence of HCV genotypes present in a biological sample comprising the steps of:

(ii) providing a sample nucleic acid,

(iii) optionally amplifying the nucleic acid with at least one primer,

(iv) hybridizing the nucleic acids of the biological sample with one or more probes according to claim 39, with said probes being optionally attached to a solid substrate,

(v) optionally washing,

(vi) detecting the hybrids formed,

(vii) inferring the presence of one or more genotypes of HCV present from the observed hybridization pattern.

24. (Previously Presented) An isolated polynucleic acid sequence consisting of 8 or more contiguous nucleotides selected from:

an HCV type 3a genomic sequence selected from the region spanning positions 417 to 957 of the Core/E1 region of HCV subtype 3a, wherein said polynucleic acid sequence is capable of hybridizing to HCV subtype 3a, but not another subtype of HCV; and

the complement of said polynucleic acid,

wherein said polynucleic acid contains at least one genotype 3a-specific nucleotide.

25. (Previously Presented) A recombinant vector comprising a vector sequence; and a prokaryotic, eukaryotic or viral promoter sequence operably linked to a polynucleic acid sequence of claim 24.

26. (Previously Presented) A kit for determining the presence of HCV genotypes comprising a polynucleic acid sequence of claim 24.

27. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the presence of a polynucleic acid sequence according to claim 24, by means of a sequencing reaction, and,

(iii) inferring from the presence of one or more of these HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

28. (Previously Presented) A method of detecting or screening for one or more HCV genotypes present in a biological sample, comprising the following steps:

(i) providing a sample nucleic acid,

(ii) specifically amplifying a polynucleic acid sequence according to claim 24, and,

(iii) inferring from the presence of one or more amplified HCV polynucleic acid sequences of step (ii) the genotype(s) present in said sample.

29. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a primer for HCV type- or subtype-specific amplification.

30. (Previously Presented) An isolated HCV polynucleic acid according to claim 24, wherein said polynucleic acid is capable of acting as a probe for HCV type- or subtype-specfic hybridization.

31. (Previously Presented) A method for detecting HCV nucleic acids present in a biological sample comprising the following steps:

(i) providing a sample nucleic acid,

(ii) determining the sequence of one or more HCV polynucleic acids according to claim 24, present in said sample.